REMARKS

The Office Action mailed October 13, 2006 has been carefully reviewed and the foregoing amendments are made in response thereto. Claims 58-74 are pending in the application and were last examined. No claims have been amended or canceled herein. In view of the amendments and the following remarks, Applicants respectfully request reconsideration and reexamination of this application and the timely allowance of the pending claims.

Objections to the Specification

In paragraph 2, the Examiner objected to the amendment filed on November 5, 2003 as introducing new matter. Applicant has amended the specification to remove the incorporation by reference of the earlier applications.

In paragraph 3, the Examiner objected to the disclosure because there are no SEQ ID Nos. in Figure 3 and on pages 37, 39, 54 and 55 of the specification. Applicants have amended the specification to add SEQ ID Nos. on pages 37, 39, 54 and 55 and have amended the BRIEF DESCRIPTION OF THE DRAWING related to Figures 3 and 4 to add SEQ ID Nos. and to correct a typographical error.

Rejections under 35 U.S.C. § 112 (first paragraph)

In paragraph 5, the Examiner rejected claims 58-74 under 35 U.S.C. §112, first paragraph, as allegedly failing to comply with the written description requirement. More specifically, the Office Action rejected the claims as allegedly incorporating new matter. Applicants respectfully disagree and submit that the specification contains sufficient teachings to demonstrate to one of ordinary skill in the art as of the filing date that

Applicants were in possession of the full scope of the claimed invention, for the reasons set forth herein.

As noted in the M.P.E.P., "an objective standard for determining compliance with the written description requirement is 'does the description clearly allow persons of ordinary skill in the art to recognize that he or she invented what is claimed.'" *See* M.P.E.P., § 2163.02 (8th Ed., Rev. No. 5) (*quoting* In re Gosteli, 872 F.2d 1008, 1012, 10 USPQ2d 1614, 1618 (Fed. Cir. 1989)). Applicants respectfully remind the Examiner that "[t]he subject matter of the claim need not be described literally (i.e., using the same terms or *in haec verba*) in order for the disclosure to satisfy the description requirement." *Id.* Furthermore, the M.P.E.P. states that "[m]ere rephrasing of a passage does not constitute new matter." *Id.* at § 2163.07.

The Examiner has raised multiple new matter rejections that all appear to rely on the Examiner's assertion that the support found in the specification for methods for selecting tag nucleic acids do not support methods for the selection of probe nucleic acids. Applicants respectfully disagree and would like to draw the Examiner's attention to the following passage from the specification at page 5, lines 6-13:

> "***In general, the selection of the tag nucleic acids facilitates selection of the probe nucleic acids***, e.g., on VLSIPS™ arrays used to monitor the tag nucleic acids by hybridization. Specifically, the probes on the array are selected for their ability to hybridize to variable sequences in the set of tag nucleic acids (the "variable" region of a tag which does not include a constant region is the entire tag). Thus, ***all of the rules for selection of tag nucleic acids can be applied to the selection of probe nucleic acids,*** for example by performing the tag selection steps and then determining the complementary set of probe nucleic acids." (emphasis added).

The application provides support for the phrase "the probes are selected to have a substantially similar melting temperature;" as recited in (b) of claim 58.

On page 3 of the office action, the Examiner indicates that although the phrase "the tag nucleic acid is selected from a group of tag nucleic acids which do not cross-hybridize and which have a substantially similar Tm" is found in the specification (see page 5, lines 31 and 32) that tag nucleic acids are different from the probes so the specification fails to provide support the phrase "the probes are selected to have a substantially similar melting temperature;" as recited in (b) of claim 58.

As discussed above, the specification teaches that the probes of the array may be selected using the same rules taught for selection of tag nucleic acids, for example, by selecting tags and then determining the complementary set of probes. The specification teaches probes that are the perfect complement of the tags. Since the specification teaches that the tags can be selected to have a substantially similar melting temperature, the specification also teaches that probes can be selected to have a substantially similar melting temperature.

The application provides support for the phrase "wherein the melting temperatures of the probes are within plus or minus 7°C".

On page 4 of the office action, the Examiner indicates that although the specification provides support for tags that have melting temperatures that are within plus or minus 7°C, (for example, in Table 1 on page 35) that this does not support the limitation of claim 59 that the melting temperature of the probes be within plus or minus 7°C. As discussed above, the specification teaches that the rules for selection of tags can be applied to the selection of probes. In addition, thermal binding stability as indicated in the specification is a measure

of the temperature-dependent stability of a nucleic acid ***duplex*** in solution and specifically, the Tm is defined as "the temperature (under defined ionic strength and pH) at which 50% of a nucleic acid (e.g., tag nucleic acid) hybridizes to a perfectly matched probe." See, page 14, lines 1-4 of the specification. It would be clear to one of skill in the art that a Tm is a characteristic of either binding partner (tag or probe) forming the duplex.

The application provides support for arrays of probes complementary to sets of tags of from 100 to 100,000, 500 to 15,000, 5,000 to 14,000 and 8,000 to 9,000 tags.

On pages 3 and 4 of the office action, the Examiner indicates that although the specification describes sets of tag nucleic acids of from 100 to 100,000, 500 to 15,000, 5,000 to 14,000 and 8,000 to 9,000 tags (see page 5, lines 16-19) that it does not support an array containing probe sets complementary to sets of tags of from 100 to 100,000, 500 to 15,000, 5,000 to 14,000 and 8,000 to 9,000 tags. As discussed above, the specification teaches that the probes of the array may be selected using the same rules taught for selection of tag nucleic acids, for example, by selecting tags and then determining the complementary set of probes. The specification teaches probes that are the perfect complement of the tags. Since the specification teaches that tags can be selected in sets of 100 to 100,000, the specification also teaches that arrays of probes complementary to sets of 100 to 100,000 tags.

In addition, the correspondence between numbers of tags and numbers of probes on the array is further supported elsewhere in the specification, for example, see page 18, lines 15-17, which describes an array with 10,000 probes complementary to 10,000 tag nucleic acids.

The application provides support for the phrase "each probe set on the array differs from every other probe set on the array by about 5 nucleotides out of 20 when aligned for maximal correspondence" as recited in claim 62.

On page 5 of the office action, the Examiner indicates that, although the specification describes that the tags differ by about 5 nucleotides out of 20, when aligned for maximal correspondence (see page 20, lines 22-24 of the specification), that it does not provide support for the limitation in claim 62 that the probes on the array differ from other probes on the array by about 5 nucleotides out of 20 when aligned for maximal correspondence. As discussed above, the specification teaches that the probes of the array may be selected using the same rules taught for selection of tag nucleic acids, for example, by selecting tags and then determining the complementary set of probes. The specification teaches probes that are the perfect complement of the tags. Since the specification teaches that tags can be selected in so that they differ from every other tag by about 5 nucleotides out of 20, the specification also teaches arrays of probes where the probes vary from all other probes on the array by about 5 nucleotides out of 20 when aligned for maximal correspondence.

The application provides support for the probe lengths recited in claims 64-66.

Finally, the Examiner indicates that although the specification on page 3, lines 29-32, provides support for ***tags*** of between 10 and 100 nucleotides, between 15 and 30 nucleotides and about 20 nucleotides that this does not support ***probes*** of between 10 and 100 nucleotides, between 15 and 30 nucleotides and about 20 nucleotides. As discussed above, the specification teaches that the probes of the array may be selected using the same rules taught for selection of tag nucleic acids, for example, by selecting tags and then determining the complementary set of probes. The specification teaches probes that are the perfect

complement of the tags. Since the specification teaches tags of the specified lengths, the specification also teaches probes of the same specified lengths.

Conclusion

In view of the foregoing amendments and remarks, Applicants respectfully request withdrawal of all outstanding rejections and early notice of allowance to that effect. Should the Examiner believe that a telephonic interview would expedite allowance of this application, he is encouraged to contact the undersigned at his convenience.

Except for issue fees payable under 37 C.F.R. § 1.18, the Commissioner is hereby authorized by this paper to charge any additional fees during the entire pendency of this application including fees due under 37 C.F.R. §§ 1.16 and 1.17 which may be required, including any required extension of time fees, or credit any overpayment to Deposit Account No.01-0431. This paragraph is intended to be a **CONSTRUCTIVE PETITION FOR EXTENSION OF TIME** in accordance with 37 C.F.R. § 1.136(a)(3).

Respectfully submitted,

Date: February 13, 2007

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